-continued

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Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser Trp Tyr Gln Gln Lys Pro
    50                  55                  60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser
65                  70                  75                  80

Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85                  90                  95

Leu Thr Ile Ser Gly Val Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
            100                 105                 110

Ala Gly Tyr Ser Ser Gly Val Ile Asp Val Ser Ala Phe Gly Gly Gly
        115                 120                 125

Thr Glu Val Val Val Lys
    130


<210> SEQ ID NO 87
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-GAA 376 variable light domain amino
      acid sequence without leader sequence

<400> SEQUENCE: 87

Ile Val Met Thr Gln Thr Pro Ser Ser Lys Ser Val Pro Val Gly Asp
1               5                   10                  15

Thr Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Val Tyr Gly Asn Asn
            20                  25                  30

Glu Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys
    50                  55                  60

Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val Glu
65                  70                  75                  80

Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Ala Gly Tyr Ser Ser Gly Val
                85                  90                  95

Ile Asp Val Ser Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys
            100                 105                 110
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1.-**42**. (canceled)

43. A method of detecting a signature peptide of Mucopolysaccharidosis Type I (MPS I) and/or Pompe Disease in a biological sample, the method comprising:

obtaining a biological sample from a subject;

digesting proteins from the biological sample with an enzyme to yield a digested biological sample comprising peptides;

enriching, from the digested biological sample comprising peptides, for:

(A) an IDUA signature peptide of MPSI of SEQ ID NO: 2 with an antibody or antigen-binding fragment thereof that binds the IDUA signature peptide and comprises: a heavy chain variable (VH) domain comprising a complementarity determining region (CDR)H1 as set forth in SEQ ID NO: 22, a CDRH2 of SEQ ID NO: 23, and a CDRH3 as set forth in SEQ ID NO: 24, and a VL domain comprising a CDRL1 as set forth in SEQ ID NO: 25, a CDRL2 as set forth in SEQ ID NO: 26, and a CDRL3 as set forth in SEQ ID NO: 27; and

a GAA signature peptide of Pompe Disease of SEQ ID NO: 5 with an antibody or antigen binding fragment thereof that binds the GAA signature peptide and comprises: a VH domain comprising a CDRH1 as set forth in SEQ ID NO: 66, a CDRH2 as set forth in SEQ ID NO: 67, and a CDRH3 as set forth in SEQ ID NO: 68, and a VL domain comprising a CDRL1 as set forth in SEQ ID NO: 69, a CDRL2 as set forth in SEQ ID NO: 70, and a CDRL3 as set forth in SEQ ID NO: 71; or

(B) a first IDUA signature peptide of MPS I of SEQ ID NO: 1 with an antibody or antigen-binding fragment thereof that binds the first IDUA signature peptide and comprises: a VH domain comprising a CDRH1 as set forth in SEQ ID NO: 10, a CDRH2 as set forth in SEQ ID NO: 11, and a CDRH3 as set forth in SEQ ID NO: 12, and a light chain variable (VL) domain